

REMARKS

Claims 1-26 have been canceled and claims 27-40 added. The newly added claims are drawn to the invention of Group VII (nucleic acid encoding leuD subunit of 3-isopropylmalate dehydratase (hydro-lyase) and host cell) of the restriction requirement mailed March 29, 2000 in the parent application, U.S. Application No. 09/173,300. No new matter is added by the addition of claims 27-40.

Entry of the amendments and favorable consideration of the claims are respectfully requested.

Respectfully submitted,



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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In showing the changes, deleted material is shown as brackets, and inserted material is shown underlined.

IN THE SPECIFICATION:

Paragraph beginning at page 1, line 3:

This application is a divisional application of U.S. Application No. 09/173,300, filed October 15, 1998, which claims the benefit of U.S. Provisional Application No. 60/063,423, filed October 28, 1997.

Paragraph beginning at page 4, line 7:

Figure 2 (A-C) depicts the amino acid sequence alignments between the dihydroxyacid dehydratase from corn clone cr1.pk0032.c4 (SEQ ID NO:2), soybean contig assembled from clones se3.pk0006.g4, and ses9c.pk001.o8 (SEQ ID NO:4), wheat clone wkm2c.pk005.c12 (SEQ ID NO:6), and *Saccharomyces cerevisiae* (NCBI gi Accession No. 1170543, SEQ ID NO:7). Amino acids which are conserved among all sequences are indicated with a plus sign (+) while those conserved only within the plant sequences are indicated by an asterisk (*).

Paragraph beginning at page 4, line 13:

Figure 3 (A-C) depicts the amino acid sequence alignments between the branched chain amino acid transaminase from corn clone cc71se-b.pk0008.b5 (SEQ ID NO:9), corn clone cen6.pk0003.b5 (SEQ ID NO:11), corn clone cta1n.pk0070.e7 (SEQ ID NO:13), rice clone rls24.pk0025.f6 (SEQ ID NO:15), soybean clone ses8w.pk0032.e9 (SEQ ID NO:17), wheat clone wlm96.pk027.n2 (SEQ ID NO:19), and *Bacillus subtilis* (NCBI gi Accession No. 1706292, SEQ ID NO:20). Amino acids which are conserved among all sequences are indicated with a plus sign (+) while those conserved only within the plant sequences are indicated by an asterisk (*).

Paragraph beginning at page 4, line 21:

Figure 4 (A-C) depicts the amino acid sequence alignments between the branched chain amino acid transaminase from rice clone rls72.pk0014.a3 (SEQ ID NO:22), soybean clone sre.pk0001.d1 (SEQ ID NO:24), soybean clone srr2c.pk003.d20 (SEQ ID NO:26), wheat clone wl1n.pk0123.c11 (SEQ ID NO:28), and *Methanococcus jannaschii* (NCBI gi Accession No. 124380, SEQ ID NO:29). Amino acids which are conserved among all sequences are indicated with a plus sign (+) while those conserved only within the plant sequences are indicated by an asterisk (*).

Paragraph beginning at page 4, line 28:

Figure 5 (A-B) depicts the amino acid sequence alignments between the branched chain amino acid transaminase from corn clone cco1.pk0030.d2 (SEQ ID NO:31), wheat clone wkm1c.pk0004.c7 (SEQ ID NO:33), and *Escherichia coli* (NCBI gi Accession

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No. 1705437, SEQ ID NO:34). Amino acids which are conserved among all sequences are indicated with a plus sign (+) while those conserved only within the plant sequences are indicated by an asterisk (*).

Paragraph beginning at page 4, line 34:

Figure 6 (A-C) depicts the amino acid sequence alignments between the *leuC* subunit of 3-isopropylmalate dehydratase from the corn contig assembled from clones cen1.pk0032.b1, cta1n.pk0077.c7, cen3n.pk0015.g3, cen3n.pk0060.h4, and cen3n.pk0121.h11 (SEQ ID NO:36), corn clone cr1n.pk0153.e9 (SEQ ID NO:38), rice clone rl0n.pk087.k16 (SEQ ID NO:40), soybean contig assembled from clones sdp3c.pk008.k13, and srm.pk0006.h5 (SEQ ID NO:42), wheat clone wre1n.pk0045.b10 (SEQ ID NO:44), and *Rhizomucor pusillus* (NCBI gi Accession No. 1708799, SEQ ID NO:45). Amino acids which are conserved among all sequences are indicated with a plus sign (+) while those conserved only within the plant sequences are indicated by an asterisk (*).

Paragraph beginning at page 5, line 5:

Figure 7 (A-B) depicts the amino acid sequence alignments between the *leuD* subunit of 3-isopropylmalate dehydratase from corn clone cr1n.pk0123.b7 (SEQ ID NO:47), rice clone rls12.pk0001.c2 (SEQ ID NO:49), soybean clone srr1c.pk003.c2 (SEQ ID NO:51), wheat clone wl1n.pk0048.a6 (SEQ ID NO:53), and *Lactococcus lactis* (NCBI gi Accession No. 400187, SEQ ID NO:54). Amino acids which are conserved among all sequences are indicated with a plus sign (+) while those conserved only within the plant sequences are indicated by an asterisk (*).

IN THE CLAIMS:

Claims 1-26 canceled.

Claims 27-40 added.

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12